Amendments to the Claims:

The following list of claims will replace all prior versions of the claims in the application:

1. (*Canceled*)

2. (*Currently amended*) A method for assessing toxicity of a compound of interest, comprising:

~~a)~~ exposing tissue samples comprising a set of genes to the compound of interest;

~~b)~~ measuring the hybridization signal of each gene in the set of genes ~~to the compound of interest~~;

~~c)~~ creating gene expression profiles using ~~two or more~~ a plurality of variables, wherein the ~~two or more~~ plurality of variables ~~include~~ includes time and dose;

identifying patterns within the gene expression profiles that demonstrate time stability and dose dependence, wherein a pattern is defined where a change in gene expression progresses in a same direction with time and increased dose, and selecting gene expression profiles that fit the patterns;

~~d)~~ creating one or more composite variables from the selected gene expression profiles ~~of (c)~~;

~~e)~~ creating one predictive composite from the composite variables ~~of (d)~~, wherein the one predictive composite comprises a binary value indicating one of a positive or negative ~~; and~~

~~f g) comparing the results of (e f) to a profile of a known compound to determine whether there is a~~ toxicological response to the compound of interest.

3. (*Previously presented*) The method of Claim 2, wherein the set of genes comprises 10-100,000 genes.

4. (*Currently amended*) The method of Claim 2, wherein the ~~two or more~~ plurality of variables further ~~include~~ includes treatment ~~6~~.

5. (*Canceled*)

6. (*Currently amended*) The method of Claim 2, wherein the step ~~(b)~~ of measuring further comprises averaging the hybridization signals of a portion of the genes having a lowest signal intensity to determine a background level; and

selecting for further analysis the hybridization signals having a difference signal intensity that ~~exceed a pre-selected percentage of~~ exceeds the background level, wherein the difference signal intensity is taken relative to a mismatch control for each gene.

7. (*Currently amended*) The method of Claim 2, wherein the step ~~(c)~~ of identifying comprises performing contrast analysis.

8. (*Currently amended*) The method of Claim 2, wherein the step ~~(c)~~ of identifying comprises performing cluster analysis.

9. (*Currently amended*) The method of Claim 2, wherein the step ~~(d)~~ of creating one or more composite variables comprises performing principal components analysis.

10. (*Currently amended*) The method of Claim 2, wherein the one predictive composite ~~variables of (c)~~ is created using logistic regression or discriminant analysis.

11. -22. (*Canceled*)

23. (*Currently amended*) The method of Claim 2, wherein the step ~~(d)~~ of creating one or more composite variables comprises performing partial least squares analysis.

24. (*Currently amended*) The method of Claim 2, wherein the step ~~(d)~~ of creating one or more composite variables comprises performing factor analysis.

25. (*Previously presented*) The method of Claim 2, wherein the compound of interest is acetaminophen.

26. (*Currently Amended*) A method for assessing the toxicity of a compound of interest, comprising:

~~a)~~ exposing tissues comprising a set of genes to the compound of interest;

~~b)~~ generating gene expression data corresponding to ~~the~~ a hybridization signal of each gene in the set of genes ~~to the compound of interest~~;

~~c)~~ identifying patterns in the gene expression data that demonstrate time stability and dose dependence, wherein a pattern is defined where a change in gene expression

progresses in a same direction with time and increased dose, and selecting a subset of the gene expression data ~~which are time-stable and dose-dependent~~ that fit the patterns;

~~d)~~ ~~combining the subset of gene expression data into~~ defining one or more composite variables ~~to assign each gene to a pattern~~ using the subset of the gene expression data; and

~~e)~~ converting the one or more composite variables into one predictive composite measure for determining a probability of similarity;

wherein the probability of similarity comprises an indicator of toxicological effect of the compound of interest.

27. (*Currently amended*) The method of claim 26, wherein the step ~~(c)~~ of identifying comprises performing contrast analysis.

28. (*Currently amended*) The method of claim 26, where the step ~~(d)~~ of defining one or more composite variables comprises performing principal components analysis.

29. (*Currently amended*) The method of claim 28, wherein the step ~~(e)~~ of converting comprises performing a logistic regression using the principal components identified in ~~step (d)~~ the principal components analysis.

30. (*Currently amended*) The method of claim 26, wherein the ~~tissue samples~~ tissues are liver, kidney, brain, spleen, pancreas and lung.

31. (*Currently amended*) The method of claim 26, wherein the step ~~(b)~~ of generating gene expression data further comprises averaging the hybridization signals of a portion of the genes having a lowest signal intensity to determine a background level; and

selecting for further analysis the hybridization signals having a difference signal intensity that ~~exceed a pre-selected percentage of~~ exceeds the background level, wherein the difference signal intensity is taken relative to a mismatch control gene for each gene.

32. (*Previously presented*) The method of Claim 2, wherein the tissue samples are liver, kidney, brain, spleen, pancreas and lung.

33. (*Previously presented*) The method of Claim 2, wherein the compound of interest is CCl_4.

34. (*New*) A method for assessing the toxicity of a compound of interest, comprising:

exposing tissues comprising a set of genes to the compound of interest;

generating gene expression data corresponding to a hybridization intensity of each gene in the set of genes;

performing analysis of variants to identify patterns in the gene expression data that demonstrate time stability and dose dependence, wherein a pattern is defined where a change in gene expression progresses in a same direction with time and increased dose;

selecting a subset of gene expression data that fits the patterns;

applying factor analysis to the subset of gene expression data to define one or more composite variables; and

applying logistic regression to convert the one or more composite variables into one predictive composite measure of toxicological effect of the compound of interest.

35. (*New*) The method of claim 34, where the step of performing an analysis of variants comprises analyzing time stability and dose dependence simultaneously.

36. (*New*) The method of claim 34, wherein the step of performing an analysis of variants comprises cluster analysis or contrast analysis.

37. (*New*) The method of claim 34, wherein the step of applying factor analysis comprises performing principal components analysis or least squares analysis.